D. Fitzgerald /646

Serial Number: 09/039,177

CRF Processing Date: 11/4/98
Edited by: _____ AH
Verified by: _____ AH (STIC staff)

[ ] Changed a file from non-ASCII to ASCII

[ ] Changed the margins in cases where the sequence text was "wrapped" down to the next line.

[ ] Edited a format error in the Current Application Data section, specifically:
_____

[ ] Edited the Current Application Data section with the actual current number. The number inputted by the applicant was [ ] the prior application data; or [ ] other _____ **ENTERED**

[ ] Added the mandatory heading and subheadings for "Current Application Data".

[ ] Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

[ ] Changed the spelling of a mandatory field (the headings or subheadings), specifically:
_____

[ ] Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
_____

[ ] Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
_____

[ ] Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

[ ] Inserted colons after headings/subheadings. Headings edited included:
_____

[ ] Deleted extra, invalid, headings used by an applicant, specifically:
_____

[ ] Deleted: [ ] non-ASCII "garbage" at the beginning/end of files; [ ] secretary initials/filename at end of file; [ ] page numbers throughout text; [ ] other invalid text, such as_____ .

[ ] Inserted mandatory headings, specifically: _____

[ ] Corrected an obvious error in the response, specifically:
_____

[ ] Edited identifiers where upper case is used but lower case is required, or vice versa.

[ ] Corrected an error in the Number of Sequences field, specifically:
_____

[✓] A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

[ ] Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

[ ] Other:
_____
_____
_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.
3/1/95

D. Fitzgerald

1646

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/039,177*

DATE: 11/04/98
TIME: 18:51:28

INPUT SET: S29620.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages. Does Not Comply
Corrected Diskette Needed

```
1                              SEQUENCE LISTING
2
3    (1)     General Information:
4
5                              (i) APPLICANT: Kohei MIYAZONO; Takeshe IMAMURA; Peter DEN
6
7                                  (ii) TITLE OF INVENTION: ISOLATED ALK-1 PROTEIN,
8                      IT, AND USES THEREOF
9
10       (iii) NUMBER OF SEQUENCES: 29
11
12       (iv) CORRESPONDENCE ADDRESS:
13                                        (A) ADDRESSEE:      Fulbright & Jaworski L.
14                              (B) STREET:     805 Third Avenue
15                                  (C) CITY:         New York City
16                              (D) STATE:      New York
17                              (E) COUNTRY:    USA
18                                  (F) ZIP:             10022
19
20       (v)   COMPUTER READABLE FORM:
21             (A) MEDIUM TYPE:  Diskette, 3.25 inch, 1.44mb
22             (B) COMPUTER:  IBM PS/2
23             (C) OPERATING SYSTEM:  PC-DOS
24             (D) SOFTWARE:  Wordperfect
25
26       (vi) CURRENT APPLICATION DATA:
27             (A) APPLICATION NUMBER: 09/039,177
28             (B) FILING DATE: March 13, 1998
29       (C) CLASSIFICATION: 435
30
31                   (vii)     PRIOR APPLICATION DATA:
32                                        (A) APPLICATION NUMBER:  PCT/GB93/0236
33             (B) FILING DATE: November 17, 1993
34
35       (vii) PRIOR APPLICATION DATA:
36             (A) APPLICATION NUMBER: GB 9224057.1
37                              (B) FILING DATE: November 17, 1992
38
39       (vii) PRIOR APPLICATION DATA:
40             (A) APPLICATION NUMBER: GB 9304677.9
41             (B) FILING DATE: March 8, 1993
42
43       (vii) PRIOR APPLICATION DATA:
44             (A) APPLICATION NUMBER: GB 9304680.3
45             (B) FILING DATE: March 8, 1993
46
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INPUT SET: S29620.raw

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47        (vii) PRIOR APPLICATION DATA:
48              (A) APPLICATION NUMBER: 9311047.6
49              (B) FILING DATE: May 28, 1993
50
51        (vii) PRIOR APPLICATION DATA:
52              (A) APPLICATION NUMBER: 9313763.6
53              (B) FILING DATE: July 2, 1993
54
55        (vii) PRIOR APPLICATION DATA:
56              (A) APPLICATION NUMBER: 9136099.2
57              (B) FILING DATE: August 3, 1993
58
59        (vii) PRIOR APPLICATION DATA:
60              (A) APPLICATION NUMBER: 321344.5
61              (B) FILING DATE: October 15, 1993
62
63        (viii) ATTORNEY/AGENT INFORMATION:
64              (A) NAME: Norman D. Hanson
65              (B) REGISTRATION NUMBER: 30,946
66              (C) REFERENCE/DOCKET NUMBER: LUD 5539 - JEL/NDH
67
68        (ix) TELECOMMUNICATION INFORMATION:
69                              (A) TELEPHONE: (212) 688-9200
70                              (B) TELEFAX:   (212) 838-3884(2) INFORMATION FOR
```

```
-->  71   (i) SEQUENCE CHARACTERISTICS:
-->  72       (A) LENGTH: 1984 base pairs
-->  73       (B) TYPE: nucleic acid
-->  74       (C) STRANDEDNESS: unknown
-->  75       (D) TOPOLOGY: linear
     76
-->  77   (ii) MOLECULE TYPE: cDNA
-->  78   (iii) HYPOTHETICAL: NO
-->  79   (iii) ANTI-SENSE: NO
-->  80    (v) FRAGMENT TYPE: internal
-->  81   (vi) ORIGINAL SOURCE:
-->  82       (A) ORGANISM: Homo sapiens
-->  83   (ix) FEATURE:
-->  84       (A) NAME/KEY: CDS
-->  85       (B) LOCATION: 283..1791
     86
-->  87   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
     88
     89   AGGAAACGGT TTATTAGGAG GGAGTGGTGG AGCTGGGCCA GGCAGGAAGA CGCTGGAATA      60
     90
     91   AGAAACATTT TTGCTCCAGC CCCCATCCCA GTCCCGGGAG GCTGCCGCGC CAGCTGCGCC     120
     92
     93   GAGCGAGCCC CTCCCCGGCT CCAGCCCGGT CCGGGGCCGC GCCGGACCCC AGCCCGCCGT     180
     94
     95   CCAGCGCTGG CGGTGCAACT GCGGCCGCGC GGTGGAGGGG AGGTGGCCCC GGTCCGCCGA     240
     96
     97   AGGCTAGCGC CCCGCCACCC GCAGAGCGGG CCCAGAGGGA CC ATG ACC TTG GGC      294
     98                                            Met Thr Leu Gly
     99                                             1
```

INPUT SET: S29620.raw

```
100
101   TCC CCC AGG AAA GGC CTT CTG ATG CTG CTG ATG GCC TTG GTG ACC CAG    342
102   Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala Leu Val Thr Gln
103    5               10                  15                      20
104
105   GGA GAC CCT GTG AAG CCG TCT CGG GGC CCG CTG GTG ACC TGC ACG TGT    390
106   Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val Thr Cys Thr Cys
107    .              25                  30                      35
108
109   GAG AGC CCA CAT TGC AAG GGG CCT ACC TGC CGG GGG GCC TGG TGC ACA    438
110   Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly Ala Trp Cys Thr
111                   40                  45                      50
112
113   GTA GTG CTG GTG CGG GAG GAG GGG AGG CAC CCC CAG GAA CAT CGG GGC    486
114   Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln Glu His Arg Gly
115               55                  60                      65
116
117   TGC GGG AAC TTG CAC AGG GAG CTC TGC AGG GGG CGC CCC ACC GAG TTC    534
118   Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg Pro Thr Glu Phe
119            70                  75                      80
120
121   GTC AAC CAC TAC TGC TGC GAC AGC CAC CTC TGC AAC CAC AAC GTG TCC    582
122   Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn His Asn Val Ser
123    85                  90                  95                      100
124
125   CTG GTG CTG GAG GCC ACC CAA CCT CCT TCG GAG CAG CCG GGA ACA GAT    630
126   Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln Pro Gly Thr Asp
127                   105                 110                     115
128
129   GGC CAG CTG GCC CTG ATC CTG GGC CCC GTG CTG GCC TTG CTG GCC CTG    678
130   Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala Leu Leu Ala Leu
131                   120                 125                     130
132
133   GTG GCC CTG GGT GTC CTG GGC CTG TGG CAT GTC CGA CGG AGG CAG GAG    726
134   Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg Arg Arg Gln Glu
135               135                 140                     145
136
137   AAG CAG CGT GGC CTG CAC AGC GAG CTG GGA GAG TCC AGT CTC ATC CTG    774
138   Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser Ser Leu Ile Leu
139            150                 155                     160
140
141   AAA GCA TCT GAG CAG GGC GAC ACG ATG TTG GGG GAC CTC CTG GAC AGT    822
142   Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp Leu Leu Asp Ser
143    165                 170                 175                     180
144
145   GAC TGC ACC ACA GGG AGT GGC TCA GGG CTC CCC TTC CTG GTG CAG AGG    870
146   Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe Leu Val Gln Arg
147                   185                 190                     195
148
149   ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC    918
150   Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val Gly Lys Gly Arg
151                   200                 205                     210
152
```

INPUT SET: S29620.raw

```
153   TAT GGC GAA GTG TGG CGG GGC TTG TGG CAC GGT GAG AGT GTG GCC GTC    966
154   Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu Ser Val Ala Val
155           215             220             225
156

157   AAG ATC TTC TCC TCG AGG GAT GAA CAG TCC TGG TTC CGG GAG ACT GAG   1014
158   Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe Arg Glu Thr Glu
159           230             235             240
160

161   ATC TAT AAC ACA GTA TTG CTC AGA CAC GAC AAC ATC CTA GGC TTC ATC   1062
162   Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile Leu Gly Phe Ile
163   245             250             255             260
164

165   GCC TCA GAC ATG ACC TCC CGC AAC TCG AGC ACG CAG CTG TGG CTC ATC   1110
166   Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln Leu Trp Leu Ile
167           265             270             275
168

169   ACG CAC TAC CAC GAG CAC GGC TCC CTC TAC GAC TTT CTG CAG AGA CAG   1158
170   Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe Leu Gln Arg Gln
171           280             285             290
172

173   ACG CTG GAG CCC CAT CTG GCT CTG AGG CTA GCT GTG TCC GCG GCA TGC   1206
174   Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val Ser Ala Ala Cys
175           295             300             305
176

177   GGC CTG GCG CAC CTG CAC GTG GAG ATC TTC GGT ACA CAG GGC AAA CCA   1254
178   Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr Gln Gly Lys Pro
179           310             315             320
180

181   GCC ATT GCC CAC CGC GAC TTC AAG AGC CGC AAT GTG CTG GTC AAG AGC   1302
182   Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val Leu Val Lys Ser
183   325             330             335             340
184

185   AAC CTG CAG TGT TGC ATC GCC GAC CTG GGC CTG GCT GTG ATG CAC TCA   1350
186   Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala Val Met His Ser
187           345             350             355
188

189   CAG GGC AGC GAT TAC CTG GAC ATC GGC AAC AAC CCG AGA GTG GGC ACC   1398
190   Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro Arg Val Gly Thr
191           360             365             370
192

193   AAG CGG TAC ATG GCA CCC GAG GTG CTG GAC GAG CAG ATC CGC ACG GAC   1446
194   Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln Ile Arg Thr Asp
195           375             380             385
196

197   TGC TTT GAG TCC TAC AAG TGG ACT GAC ATC TGG GCC TTT GGC CTG GTG   1494
198   Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe Gly Leu Val
199           390             395             400
200

201   CTG TGG GAG ATT GCC CGC CGG ACC ATC GTG AAT GGC ATC GTG GAG GAC   1542
202   Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly Ile Val Glu Asp
203   405             410             415             420
204

205   TAT AGA CCA CCC TTC TAT GAT GTG GTG CCC AAT GAC CCC AGC TTT GAG   1590
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INPUT SET: S29620.raw

```
206    Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp Pro Ser Phe Glu
207                    425             430             435
208
209    GAC ATG AAG AAG GTG GTG TGT GTG GAT CAG CAG ACC CCC ACC ATC CCT    1638
210    Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro Thr Ile Pro
211                440             445             450
212
213    AAC CGG CTG GCT GCA GAC CCG GTC CTC TCA GGC CTA GCT CAG ATG ATG    1686
214    Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala Gln Met Met
215            455             460             465
216
217    CGG GAG TGC TGG TAC CCA AAC CCC TCT GCC CGA CTC ACC GCG CTG CGG    1734
218    Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg
219        470             475             480
220
221    ATC AAG AAG ACA CTA CAA AAA ATT AGC AAC AGT CCA GAG AAG CCT AAA    1782
222    Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro Glu Lys Pro Lys
223    485             490             495             500
224
225    GTG ATT CAA TAGCCCAGGA GCACCTGATT CCTTTCTGCC TGCAGGGGGC            1831
226    Val Ile Gln
227
228    TGGGGGGGTG GGGGGCAGTG GATGGTGCCC TATCTGGGTA GAGGTAGTGT GAGTGTGGTG   1891
229
230    TGTGCTGGGG ATGGGCAGCT GCGCCTGCCT GCTCGGCCCC CAGCCCACCC AGCCAAAAAT   1951
231
232    ACAGCTGGGC TGAAACCTGA AAAAAAAAAA AAA                               1984
233
234    (2) INFORMATION FOR SEQ ID NO: 2:
235        (i) SEQUENCE CHARACTERISTICS:
236            (A) LENGTH: 503 amino acids
237            (B) TYPE: amino acid
238            (D) TOPOLOGY: linear
239        (ii) MOLECULE TYPE: protein
240
241        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
242
243    Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala
244    1               5               10              15
245
246    Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val
247                20              25              30
248
249    Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly
250            35              40              45
251
252    Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln
253        50              55              60
254
255    Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg
256    65              70              75              80
257
258    Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/039,177*

INPUT SET: S29620.raw

Line	Error	Original Text
10	Number of Sequences (29) Doesn't Equal Actual Count (28)	(iii) NUMBER OF SEQUENCES: 29
29	Wrong Classification	(C) CLASSIFICATION: 435
71	Unknown or Misplaced Identifier	(i) SEQUENCE CHARACTERISTICS:
72	Unknown or Misplaced Identifier	(A) LENGTH: 1984 base pairs
73	Unknown or Misplaced Identifier	(B) TYPE: nucleic acid
74	Unknown or Misplaced Identifier	(C) STRANDEDNESS: unknown
75	Unknown or Misplaced Identifier	(D) TOPOLOGY: linear
77	Unknown or Misplaced Identifier	(ii) MOLECULE TYPE: cDNA
78	Unknown or Misplaced Identifier	(iii) HYPOTHETICAL: NO
79	Unknown or Misplaced Identifier	(iii) ANTI-SENSE: NO
80	Unknown or Misplaced Identifier	(v) FRAGMENT TYPE: internal
81	Unknown or Misplaced Identifier	(vi) ORIGINAL SOURCE:
82	Unknown or Misplaced Identifier	(A) ORGANISM: Homo sapiens
83	Unknown or Misplaced Identifier	(ix) FEATURE:
84	Unknown or Misplaced Identifier	(A) NAME/KEY: CDS
85	Unknown or Misplaced Identifier	(B) LOCATION: 283..1791
87	Unknown or Misplaced Identifier	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1: